FIG. 1A

```
  1 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC
    CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG
  1                      M   S   Q   R   E   G   S   L   E   D   H

 51 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC
    TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG
 12  Q   T   D   S   S   I   S   F   L   P   H   L   E   A   K   I

101 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT
    GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA
 28  R   Q   T   H   N   L   A   R   L   L   T   K   Y   A   E   Q   L

151 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT
    AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA
 45  L   E   E   Y   V   Q   Q   Q   G   E   P   F   G   L   P   G   F

201 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC
    AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG
 62  S   P   P   R   L   P   L   A   G   L   S   G   P   A   P   S

251 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT
    GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA
 78  H   A   G   L   P   V   S   E   R   L   R   Q   D   A   A   A   L

301 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC
    CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG
 95  S   V   L   P   A   L   L   D   A   V   R   R   R   Q   A   E   L

351 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC
    ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG
112  N   P   R   A   P   R   L   L   R   S   L   E   D   A   A   R

401 CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG
    GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC
128  Q   V   R   A   L   G   A   A   V   E   T   V   L   A   A   L   G

451 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT
    GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA
145  A   A   A   R   G   P   G   P   E   P   V   T   V   A   T   L   F

501 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC
    AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG
162  T   A   N   S   T   A   G   I   F   S   A   K   V   L   G   F

551 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT
    GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA
178  H   V   C   G   L   Y   G   E   W   V   S   R   T   E   G   D   L

601 GGGCCAGCTG GTGCCAGGGG CGTCGCCTG AGAGTGAATA CTTTTTCTTG
    CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC
195  G   Q   L   V   P   G   G   V   A   O
```

FIG. 1B

```
 651  TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT
      ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA

 701  CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG
      GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC

 751  TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT
      AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA

 801  TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC
      AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG

 851  TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT
      AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA

 901  GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG
      CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC

 951  GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG
      CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC

1001  CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT
      GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA

1051  GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT
      CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA

1101  TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA
      AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT

1151  AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC
      TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG

1201  TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA
      AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT

1251  GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT
      CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA

1301  AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA
      TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT

1351  AA (polyA)
      TT
```

FIG. 2

```
                    10        20        30        40        50
chf.781   MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQ
                              **            ***           *  * **
humcntf           MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK
                          10        20        30        40


                    60        70        80        90       100
chf.781   QQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL
          **          *       *  *                ***       *      *
humcntf   HQGLNKNINLDSADGMPVA----STDQWSELTEAERLQENLQAYRTFHVL
            50        60        70        80


                   110       120       130       140
chf.781   LD-AVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARG
           *       *       *           ** *      *        *
humcntf   LARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPR
            90       100       110       120       130


        150       160       170       180       190
chf.781   PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP
                      *  *   *   *   *         *   *    **
humcntf   NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS
            140       150       160       170       180


           200
chf.781   GGVAO

humcntf   SHQTGIPARGSHYIANNKKM
                    190       200
```

FIG. 3

PHENYLEPHRINE (uM)　　293 TRANSFECTION
STANDARD CURVE

FIG. 4

FIG. 5A

```
  1  GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA
     CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT
  1                                    M  S  R   R  E  G


 51  AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT
     TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA
  7   S  L  E  D  P  Q  T  D  S  S   V  S  L  L  P  H  L


101  GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT
     CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA
 24   E  A  K  I  R  Q  T  H  S  L   A  H  L  L  T  K  Y


151  ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC
     TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG
 41   A  E  Q  L  L  Q  E  Y  V  Q   L  Q  G  D  P  F


201  GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC
     CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG
 57   G  L  P  S  F  S  P  P  R  L   P  V  A  G  L  S  A


251  CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG
     GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC
 74   P  A  P  S  H  A  G  L  P  V   H  E  R  L  R  L  D


301  ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC
     TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG
 91   A  A  A  L  A  A  L  P  P  L   L  D  A  V  C  R


351  CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA
     GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT
107   R  Q  A  E  L  N  P  R  A  P   R  L  L  R  R  L  E


401  GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC
     CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG
124   D  A  A  R  Q  A  R  A  L  G   A  A  V  E  A  L  L


451  TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCGCC
     ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG
141   A  A  L  G  A  A  N  R  G  P   R  A  E  P  P  A
```
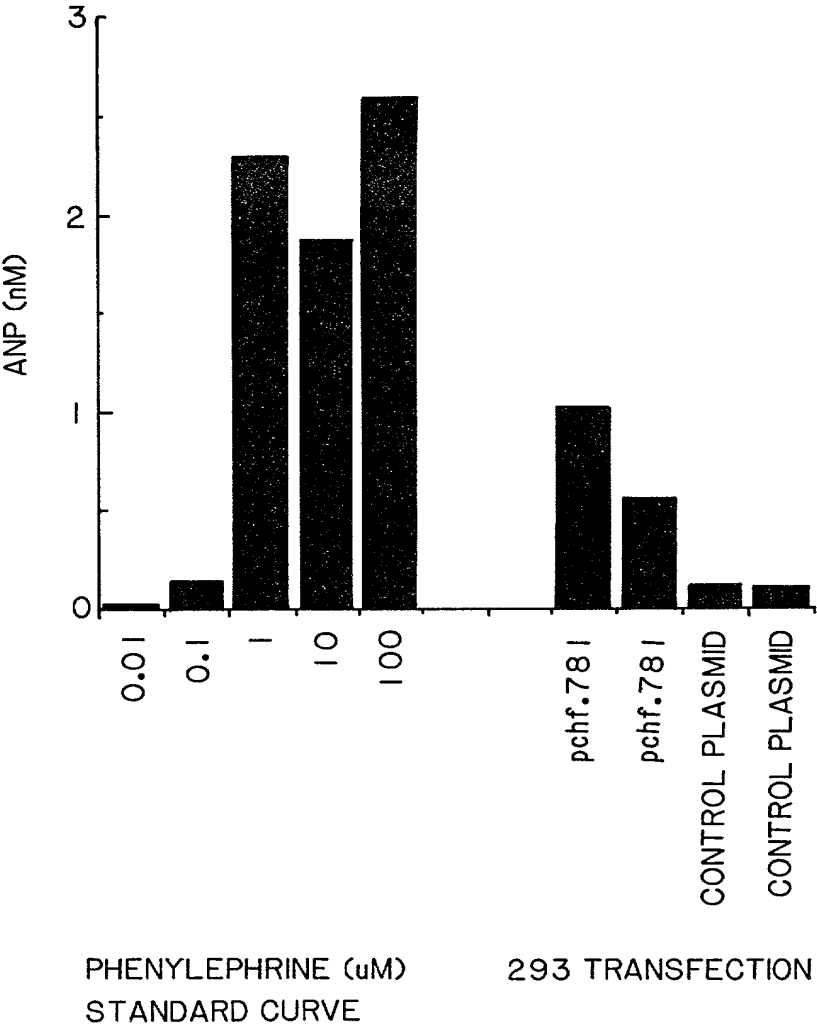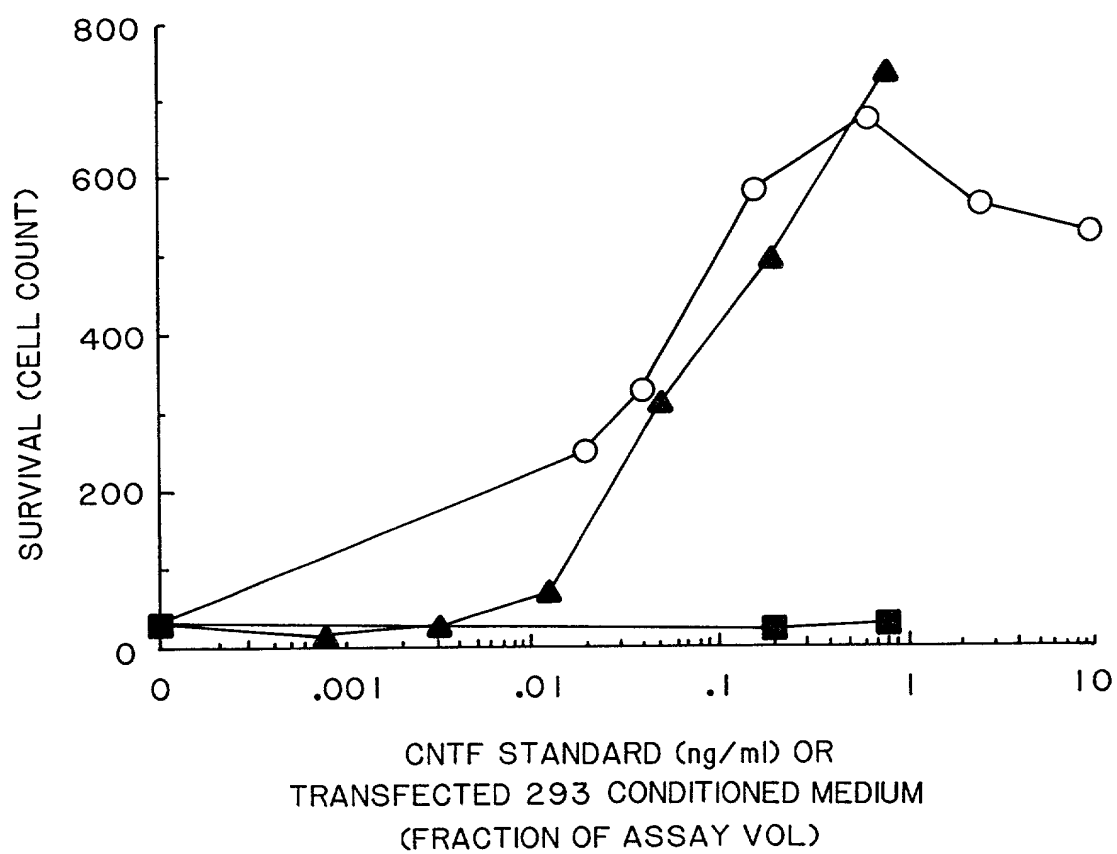
FIG. 5B

```
501    GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT
       CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA
157    A  T  A  S  A  A  S  A  T  G  V  F  P  A  K  V  L


551    GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG
       CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC
174     G  L  R  V  C  G  L  Y  R  E  W  L  S  R  T  E  G


601    GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC
       CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG
191     D  L  G  Q  L  L  P  G  G  S  A  O


651    AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT
       TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA


701    GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC
       CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG


751    ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC
       TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG


801    AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC
       TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG


851    AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC
       TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG


901    AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA
       TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT


951    TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT
       AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA


1001   CCGGGGCTCA AGCGATCC
       GGCCCCGAGT TCGCTAGG
```

FIG. 6

```
humct1     1   MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLLTKYAEQLLQEYVQLQG
               **  ******* ***** * ************ ** ********** **** **
chf.781    1   MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG


humct1    54   DPFGLPSFSPPRLPVAGLSAPAPSHAGLPVHERLRLDAAALAALPPLLDAVCR
               ***** ******* **** ********** **** *****   ** ***** *
chf.781   54   EPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR


humct1   107   RQAELNPRAPRLLRRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
               ************** ****** ** *******  ****** ***    **
chf.781  107   RQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTVAT


humct1   160   --SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
               *  *   * * *****  ***** ** ********** *** *
chf.781  160   LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA
```